Docket No. 1134C

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant:	Duvick, et al.	Date:	April 17, 2001
Serial No.:	09/771,045	Group Art Unit:	1633
Filed	January 26, 2001	Examiner:	

For: "Amino Polyol Amine Oxidase Polynucleotides and Related Polypeptides and Methods of Use"

Assistant Commissioner for Patents
Washington, D.C. 20231

TRANSMITTAL

Transmitted herewith are the following documents: Response to Notice to Comply; Substitute computer readable form (CFR) copy of the Sequence Listing; Substitute paper copy of Sequence Listing; and Statement to Support Filing and Submission in Accordance with 37 CFR §§1.821 through 1.825.

Although there should be no fees associated with the filing of these documents the Commissioner is hereby authorized to charge any processing fees associated with said documents, or to credit any overpayment, to Deposit Account 16-1852. A duplicate copy of this sheet is enclosed.

Respectfully submitted,

Karen Moon Bruce
Agent for Applicant(s)
Registration No. 42,366

PIONEER HI-BRED INTERNATIONAL, INC.
Corporate Intellectual Property
7100 N.W. 62nd Avenue
P.O. Box 1000
Johnston, Iowa 50131-1000
Phone: (515) 248-4879
Facsimile: (515) 334-6883

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RESPONSE TO NOTICE TO COMPLY WITH REQUIREMENTS
FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE
AND/OR AMINO ACID SEQUENCE DISCLOSURES

This letter is in response to the "Notice to Comply" mailed on March 29, 2001 which

indicated that the copy of the "Sequence Listing" in computer readable form does not comply

with the requirements of 37 C.F.R. 1.822 and/or 1.823. A copy of "The Notice to Comply" is

enclosed.

Enclosed please find a substitute computer readable form (CFR) copy of the

"Sequence Listing", a substitute paper copy of the "Sequence Listing", and a statement that

the content of the paper and computer readable copies are the same, and where applicable,

include no new matter.
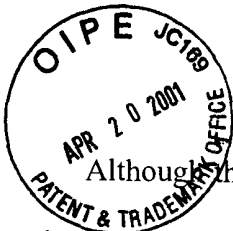
Although there should be no fees associated with this Response the Commissioner is hereby authorized to charge any processing fees associated with said Response, or to credit any overpayment, to Deposit Account 16-1852.

Respectfully submitted,

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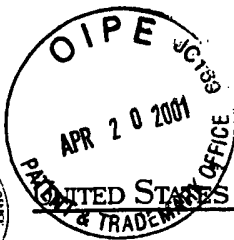
RECEIVED

APR 2 4 2001

UNITED STATES PATENT AND TRADEMARK OFFICE

COMMISSIONER FOR PATENTS
UNITED STATES PATENT AND TRADEMARK OFFICE
TECH CENTER 1600/2900

APPLICATION NUMBER	FILING/RECEIPT DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NUMBER
09/771,045	01/26/2001	Jonathan P. Duvick	1134C

CONFIRMATION NO. 7253

FORMALITIES LETTER

OC000000005917489

Pioneer Hi-Bred International, Inc.
Corporate Intellectual Property
7100 N.W. 62nd Avenue
P.O. Box 1000
Johnston, IA 50131-1000

Date Mailed: 03/29/2001

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant is given TWO MONTHS FROM THE DATE OF THIS NOTICE within which to file the items indicated below to avoid abandonment. Extensions of time may be obtained under the provisions of 37 CFR 1.136(a).

- A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing." Applicant must provide a substitute computer readable form (CRF) copy of the "Sequence Listing" and a statement that the content of the sequence listing information recorded in computer readable form is identical to the written (on paper or compact disc) sequence listing and, where applicable, includes no new matter, as required by 37 CFR 1.821(e), 1.821(f), 1.821(g), 1.825(b), or 1.825(d).

For questions regarding compliance to these requirements, please contact:

- **For Rules Interpretation, call (703) 308-4216**
- **To Purchase PatentIn Software, call (703) 306-2600**
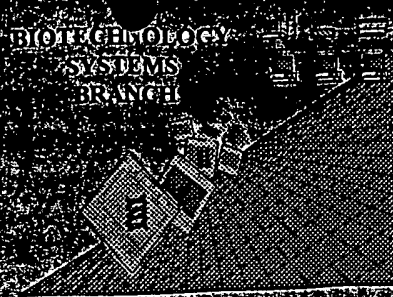- **For PatentIn Software Program Help, call (703) 306-4119 or e-mail at patin21help@uspto.gov or patin3help@uspto.gov**

A copy of this notice MUST be returned with the reply.

Customer Service Center
Initial Patent Examination Division (703) 308-1202
PART 1 - ATTORNEY/APPLICANT COPY

RAW SEQUENCE LISTING
ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: __09/771,045__

Source: __OIPE__

Date Processed by STIC: __2/8/2001__

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE __CHECKER VERSION 3.0 PROGRAM__ ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
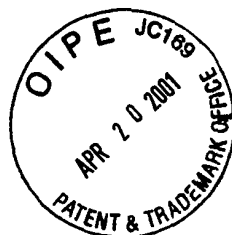
http://www.uspto.gov/web/offices/pac/checker

OIPE

RAW SEQUENCE LISTING   DATE: 02/08/2001
PATENT APPLICATION: US/09/771,045   TIME: 12:14:08

Input Set : A:\1134CSEQLIST.TXT
Output Set: N:\CRF3\02082001\I771045.raw

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     4 <110> APPLICANT: Duvick, Jonathan P.
     5        Gilliam, Jacob T.
     6        Maddox, Joyce R.
     8 <120> TITLE OF INVENTION: Amino Polyol Amine Oxidase
     9        Polynucleotides and Related Polypeptides and Methods of Use
    12 <130> FILE REFERENCE: 1134C
C-->14 <140> CURRENT APPLICATION NUMBER: US/09/771,045
C-->14 <141> CURRENT FILING DATE: 2001-01-26
    14 <150> PRIOR APPLICATION NUMBER: US 60/092,936
    15 <151> PRIOR FILING DATE: 1998-07-15
    17 <150> PRIOR APPLICATION NUMBER: US 60/135,391
    18 <151> PRIOR FILING DATE: 1999-05-21
    20 <150> PRIOR APPLICATION NUMBER: US 09/352,159
    21 <151> PRIOR FILING DATE: 1999-07-12
    23 <150> PRIOR APPLICATION NUMBER: US 09/352,168
    24 <151> PRIOR FILING DATE: 1999-07-12
    26 <160> NUMBER OF SEQ ID NOS: 53
    28 <170> SOFTWARE: FastSEQ for Windows Version 3.0
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    33 <213> ORGANISM: Exophiala spinifera
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    38 <223> OTHER INFORMATION: n = A,T,C or G
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    43  attgtcgatc gacgtcgatg ctggtatctc tggcaaatga gatggggtca cagctcgatt   180
    44  ggaggacgcc cgagaagcct tgttcgcgcc accacggctt gtcccatacg aagactatct   240
    45  tgctatagta gcccaggata gaattttccg ccaatgcttg cttctcggcg ggaagaggtg   300
    46  gtgaaaatgt caaggtggga tacaaggttg tcggtaacga aaccancacc tttttgcttc   360
    47  ggaacacggc gc                                                       372
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    50 <211> LENGTH: 182
    51 <212> TYPE: DNA
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    56  tacaaggttg tcggtaacga aaccaccacc tttttgcttc ggaacacggc gcccgaggcc   120
    57  gatcgtactg tacagccgga tgccgactgc tcaatttcag cgacgggggt gttgaggtgc   180
    58  ac                                                                  182
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    61 <211> LENGTH: 29
    62 <212> TYPE: DNA
    63 <213> ORGANISM: Artificial Sequence
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RAW SEQUENCE LISTING   DATE: 02/08/2001
PATENT APPLICATION: US/09/771,045   TIME: 12:14:08

Input Set : A:\1134CSEQLIST.TXT
Output Set: N:\CRF3\02082001\I771045.raw

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66  <223> OTHER INFORMATION: Designed oligonucleotide for 3' RACE, N21965
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73  <211> LENGTH: 28
74  <212> TYPE: DNA
75  <213> ORGANISM: Artificial Sequence
77  <220> FEATURE:
78  <223> OTHER INFORMATION: Designed oligonucleotide for 5' RACE, 21968
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83  <210> SEQ ID NO: 5
84  <211> LENGTH: 1389
85  <212> TYPE: DNA
86  <213> ORGANISM: Exophiala spinifera
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90  <222> LOCATION: (1)...(1386)
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95   1               5                   10                  15
97   gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt    96
98   Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu
99               20                  25                  30
101  gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt   144
102  Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
103          35                  40                  45
105  ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac   192
106  Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
107      50                  55                  60
109  agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag   240
110  Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
111  65                  70                  75                  80
113  ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac   288
114  Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
115              85                  90                  95
117  ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag   336
118  Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
119              100                 105                 110
121  gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc   384
122  Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile
123          115                 120                 125
125  gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg   432
126  Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg
127      130                 135                 140
129  ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg   480
130  Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu
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131 145                  150                  155                  160
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135                  165                  170                  175
137 gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag      576
138 Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys
139                  180                  185                  190
141 agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg      624
142 Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly
143                  195                  200                  205
145 cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc atg      672
146 Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met
147     210                  215                  220
149 tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct      720
150 Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala
151 225                  230                  235                  240
153 gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc      768
154 Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly
155                  245                  250                  255
157 gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg      816
158 Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu
159                  260                  265                  270
161 tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca      864
162 Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala
163     275                  280                  285
165 ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta      912
166 Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val
167     290                  295                  300
169 tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa      960
170 Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln
171 305                  310                  315                  320
173 tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc     1008
174 Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val
175                  325                  330                  335
177 gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cgg     1056
178 Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg
179                  340                  345                  350
181 aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac     1104
182 Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp
183     355                  360                  365
185 caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg     1152
186 Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro
187     370                  375                  380
189 gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga     1200
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191 385                  390                  395                  400
193 gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg     1248
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Input Set : A:\1134CSEQLIST.TXT
Output Set: N:\CRF3\02082001\I771045.raw

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199              420             425             430

201  tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa       1344
202  Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln
203              435             440             445

205  cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca             1386
206  Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
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213  <212> TYPE: PRT
214  <213> ORGANISM: Exophiala spinifera
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221  Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
222          35              40              45
223  Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
224          50              55              60
225  Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
226  65              70              75              80
227  Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
228              85              90              95
229  Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
230              100             105             110
231  Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile
232          115             120             125
233  Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg
234          130             135             140
235  Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu
236  145             150             155             160
237  Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly
238              165             170             175
239  Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys
240              180             185             190
241  Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly
242          195             200             205
243  Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met
244          210             215             220
245  Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala
246  225             230             235             240
247  Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly
248              245             250             255
249  Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu
250          260             265             270
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251  Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala
252          275             280             285
253  Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val
254          290             295             300
255  Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln
256  305             310             315             320
257  Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val
258              325             330             335
259  Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg
260          340             345             350
261  Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp
262          355             360             365
263  Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro
264          370             375             380
365  Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly
266  385             390             395             400
267  Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser
268              405             410             415
269  Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr
270          420             425             430
271  Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln
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279  <213> ORGANISM: Exophiala spinifera
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294  1               5                   10                  15
296  gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt    96
297  Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu
298          20              25              30
300  gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt   144
301  Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
302          35              40              45
304  ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac   192
305  Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
306  50              55              60
308  agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag   240
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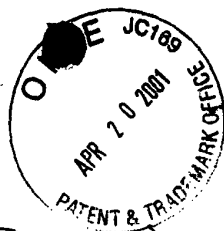
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  <211> 692
  <212> PRT
  <213> Unknown
  <400> 19
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see Item 12 on Ena Summary Sheet

The types of errors shown exist <u>throughout</u> the Sequence Listing. Please check subsequent sequences for similar errors.

FYI

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:46 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:349 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 7
L:1234 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1234 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
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L:2517 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
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L:3154 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:3487 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:3487 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:3810 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:3810 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:4186 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39
L:4247 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40
```
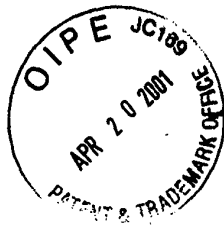
Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length
Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.

8 _____ Skipped Sequences (OLD RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism (NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.

19 and more

12 _√_ Use of <220>Feature (NEW RULES)
Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.